



#9

COPY OF PAPERS
ORIGINALLY FILED

SEQUENCE LISTING

<110> RASTELLI, LUCA

<120> NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
SAME

<130> 10716-08

<140> 09/784,810

<141> 2001-02-14

<150> 60/182,360

<151> 2000-02-14

<150> 60/191,261

<151> 2000-03-22

<160> 29

<170> PatentIn Ver. 2.1

<210> 1

<211> 1600

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1)

<223> a, t, c, g, other or unknown

<400> 1

```
nccccccggg gctcctatag ccacggctcc gggcggggaa ggcgagcccc acagccggcc 60
ctgcgacgcc cgcctgggca gcaccgataa ggagctgaag gcaggagccg ccgccacggg 120
cagcgcccc acagcgccag ggacccccctg gcagcgggag ccgcgggtcg aggttatgga 180
tccagcgggc ggccccggg gcgtgctccc gcggccctgc cgcgtgctgg tgctgctgaa 240
cccgcgcggc ggcaagggca aggccttgca gctcttcgg agtcacgtgc agcccccttt 300
ggctgaggct gaaatctcct tcacgctgat gctcactgag cggcggaacc acgcgcggga 360
gctgggtgcg tcggaggagc tgggcccgtg ggacgctctg gtggtcatgt ctggagacgg 420
gctgatgcac gaggtggtga acgggctcat ggagcggcct gactgggaga ccgccatcca 480
gaagccccctg tgtagcctcc cagcaggctc tggcaacgcg ctggcagctt ccttgaacca 540
ttatgctggc tatgagcagg tcaccaatga agacctcctg accaactgca cgctattgct 600
gtgcccggcg gtgctgtcac ccatgaacct gctgtctctg cacacggctt cggggctggc 660
ctcgttctct gtgctcagcc tggcctgggg ctctcattgct gatgtggacc tagagagtga 720
taagtatcgg cgtctggggg agatgcgctt cactctgggc accttctgc gtctggcagc 780
cctgcgcacc taccgcggcc gactggctac cctccctgta ggaagagtgg gtttcaagac 840
acctgcttcc ccggttgtgg tccagcaggg ccggttagat gcacacctgg tgccactgga 900
ggagcaggtg ccttctcact ggcaggtggt gcccgacgag gactttgtgc tagtcctggc 960
actgctgcac tcgcacctgg ccagtgaagt gtttgctgca cccatggggc gctgtgcagc 1020
tggcgctatg cactctgtct acgtgcgggc gggagtgtct cgtgctatgc tgcctggcct 1080
cttccctggc atggagaagg gcaggcatat ggagtatgaa tggccctact tggatatagt 1140
gcccgtggtc gccctccgct tggagcccaa ggtgtgtttg cagtggatgg 1200
ggaattgatg gttagcgagg ccgtgcaggg ccaggtgcac ccaaactact tctggatggg 1260
cagcgggttc gtggagcccc cgcgccagct gaagccccag cagatgccac cgccagaaga 1320
gcccttatga cccctggggc gcgctgtgcc ttagtgtcta ctgcaggac ccttccctct 1380
tccctagggc tgcaggccct gtccacagct cctgtggggg tggaggagac tccctcggag 1440
aagcgtgaga aggtggaggc tatgctttgg gggacaggc cagaatgaag tccctgggtca 1500
```

ggagcccagc tggtgggcc cagctgccta tgtaaggcct tctagtttgt tctgagaccc 1560
ccaccccacg aaccaaattcc aaataaagtg acattcccaa 1600

<210> 2
<211> 384
<212> PRT
<213> Homo sapiens

<400> 2
Met Asp Pro Ala Gly Gly Pro Arg Gly Val Leu Pro Arg Pro Cys Arg
1 5 10 15
Val Leu Val Leu Leu Asn Pro Arg Gly Gly Lys Gly Lys Ala Leu Gln
20 25 30
Leu Phe Arg Ser His Val Gln Pro Leu Leu Ala Glu Ala Glu Ile Ser
35 40 45
Phe Thr Leu Met Leu Thr Glu Arg Arg Asn His Ala Arg Glu Leu Val
50 55 60
Arg Ser Glu Glu Leu Gly Arg Trp Asp Ala Leu Val Val Met Ser Gly
65 70 75 80
Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
85 90 95
Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Ala Gly Ser
100 105 110
Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr Ala Gly Tyr Glu Gln
115 120 125
Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr Leu Leu Leu Cys Arg
130 135 140
Pro Val Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
145 150 155 160
Leu Arg Ser Phe Ser Val Leu Ser Leu Ala Trp Gly Phe Ile Ala Asp
165 170 175
Val Asp Leu Glu Ser Asp Lys Tyr Arg Arg Leu Gly Glu Met Arg Phe
180 185 190
Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu Arg Thr Tyr Arg Gly
195 200 205
Arg Leu Ala Thr Leu Pro Val Gly Arg Val Gly Phe Lys Thr Pro Ala
210 215 220
Ser Pro Val Val Val Gln Gln Gly Pro Val Asp Ala His Leu Val Pro
225 230 235 240
Leu Glu Glu Gln Val Pro Ser His Trp Gln Val Val Pro Asp Glu Asp
245 250 255

Phe Val Leu Val Leu Ala Leu Leu His Ser His Leu Ala Ser Glu Met
 260 265 270

Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly Val Met His Leu Phe
 275 280 285

Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu Leu Arg Leu Phe Leu
 290 295 300

Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu Cys Pro Tyr Leu Val
 305 310 315 320

Tyr Val Pro Val Val Ala Phe Arg Leu Glu Pro Lys Asp Gly Lys Gly
 325 330 335

Val Phe Ala Val Asp Gly Glu Leu Met Val Ser Glu Ala Val Gln Gly
 340 345 350

Gln Val His Pro Asn Tyr Phe Trp Met Val Ser Gly Cys Val Glu Pro
 355 360 365

Pro Pro Ser Trp Lys Pro Gln Gln Met Pro Pro Pro Glu Glu Pro Leu
 370 375 380

<210> 3

<211> 1759

<212> DNA

<213> Mus musculus

<400> 3

gaactccagg gtcctctggt agagaagcca ccttcaaggc gtgacctagt tcaactgcaat 60
 cctttcttat ctgggttcgt tttcctcttg gactcgcttc ttctggactt taagaagcga 120
 tgcgaagata gagatctggc cgccccgggg aatgacgagg gcgctcacac agcccaggga 180
 ggtggagagg gcgagccac ggccagtcgc cagacaccct cctgggcaac accgataaga 240
 agctgaacgc aggagccgcc gttacctcta gcagcgccgg ggcagcaccg gtggccctt 300
 gtcagcggga gcccgggac ctggctatgg aaccagtaga atgccctcga ggactgctcc 360
 cacggccatg cagagtgtg gtgctgtga acccccaggg tggcaagggc aaggctctgc 420
 agctcttcca gagccgtgtg cagcccttcc tggaggaggc agagataacc tttaaactga 480
 tactcaccga acggaagaac catgccaggg agctgggtgtg tgcagaggag ttgggtcact 540
 gggacgcctt ggcagtcag tccgggtgat gtctgatgca tgaagtgtg aatgggctaa 600
 tggaaacggc agactgggag actgccatcc agaaaccctt gctagcctc cctggaggct 660
 ccggcaatgc gctggcagct tctgtgaacc actatgctgg gtacgagcag gtgaccaatg 720
 aagacctgct catcaactgc aactgctgt tgtgccgccg gcgcctgtca cccatgaacc 780
 tgctgtccct gcacactgct tctgggctgc ggctctattc tgtgctcagt ctgtctggg 840
 gctttgttgc tgacgtggac ctcgagagtg agaagtagac gcgcttgggg gagattcggt 900
 tcacagtggg caccttcttt cgcttagcaa gcctgcgcat ctaccaaggc caactggcct 960
 accttctgtt aggaactgtg gcctctaaga gaccgcctc tacactggtg cagaagggcc 1020
 ccgtcgacac acacttgtt cctctggagg agccagtgcc ttctcattgg actgtggtac 1080
 cagaacagga cttcgtctg gtgctggtgc tgctacacac ccacctgagc tccgagctgt 1140
 ttgcagcacc catgggccgc tgtgaggctg gtgttatgca tctgttctac gtacgtgcgg 1200
 ggggtgtcaag ggctgcgctg ctgcccctct tctgggcat gcagaagggc aagcatatgg 1260
 aacttgactg tccatacctg gtccatgtgc ccgtgggtgc tttccgcctg gagcccagga 1320
 gccagagggg cgtgttttct gtggatggag agctgatggt atgtgaagct gtgcagggcc 1380
 aagtgcaccc aaactacctt tggatggtct gtggcagcag agatgcccc a tccggccggg 1440
 actccccggg ggggcccact ccagaagaac cataactctg tgcccttct tactctgtct 1500
 aggctgagat gggaccctcc cccgcaccca cctcctggta tgggagggtta tttctaaagt 1560

tcctatggaa gtggtgggga cccctgcaga gaaagctaga aggtggggct atgacttggga 1620
aagaaaggct ttaccttcca gttagagtaa catccccagt agagccctgc tggctggacc 1680
agttgcatat agaagacatt cccattgct tttagggacc ttccctggga accaaattca 1740
aataaagaga cttttccaa 1759

<210> 4
<211> 382
<212> PRT
<213> Mus musculus

<400> 4
Met Glu Pro Val Glu Cys Pro Arg Gly Leu Leu Pro Arg Pro Cys Arg
1 5 10 15
Val Leu Val Leu Leu Asn Pro Gln Gly Gly Lys Gly Lys Ala Leu Gln
20 25 30
Leu Phe Gln Ser Arg Val Gln Pro Phe Leu Glu Glu Ala Glu Ile Thr
35 40 45
Phe Lys Leu Ile Leu Thr Glu Arg Lys Asn His Ala Arg Glu Leu Val
50 55 60
Cys Ala Glu Glu Leu Gly His Trp Asp Ala Leu Ala Val Met Ser Gly
65 70 75 80
Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
85 90 95
Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Gly Gly Ser
100 105 110
Gly Asn Ala Leu Ala Ala Ser Val Asn His Tyr Ala Gly Tyr Glu Gln
115 120 125
Val Thr Asn Glu Asp Leu Leu Ile Asn Cys Thr Leu Leu Leu Cys Arg
130 135 140
Arg Arg Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
145 150 155 160
Leu Arg Leu Tyr Ser Val Leu Ser Leu Ser Trp Gly Phe Val Ala Asp
165 170 175
Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu Gly Glu Ile Arg Phe
180 185 190
Thr Val Gly Thr Phe Phe Arg Leu Ala Ser Leu Arg Ile Tyr Gln Gly
195 200 205
Gln Leu Ala Tyr Leu Pro Val Gly Thr Val Ala Ser Lys Arg Pro Ala
210 215 220
Ser Thr Leu Val Gln Lys Gly Pro Val Asp Thr His Leu Val Pro Leu
225 230 235 240
Glu Glu Pro Val Pro Ser His Trp Thr Val Val Pro Glu Gln Asp Phe

	245		250		255
Val Leu Val	Leu Val Leu Leu His	Thr His Leu	Ser Ser Glu	Leu Phe	
	260		265		270
Ala Ala Pro	Met Gly Arg Cys Glu	Ala Gly Val	Met His Leu	Phe Tyr	
	275		280		285
Val Arg Ala	Gly Val Ser Arg Ala	Ala Leu Leu	Arg Leu Phe	Leu Ala	
	290		295		300
Met Gln Lys	Gly Lys His Met Glu	Leu Asp Cys	Pro Tyr Leu	Val His	
	305		310		315
Val Pro Val	Val Ala Phe Arg Leu	Glu Pro Arg	Ser Gln Arg	Gly Val	
	325		330		335
Phe Ser Val	Asp Gly Glu Leu Met	Val Cys Glu	Ala Val Gln	Gly Gln	
	340		345		350
Val His Pro	Asn Tyr Leu Trp Met	Val Cys Gly	Ser Arg Asp	Ala Pro	
	355		360		365
Ser Gly Arg	Asp Ser Arg Arg Gly	Pro Pro Pro	Glu Glu Pro		
	370		375		380

<210> 5
 <211> 1840
 <212> DNA
 <213> Homo sapiens

<400> 5
 gccggcgccc ccggcgcgga tgctgtctct gtgctgttat ctgagatcat cgccgttgag 60
 gaaacagacg ttcacgggaa acatcaaggc agtggaaaat ggcagaaaat ggaaaagcct 120
 tacgctttta cagttcactg tgtaaagaga gcacgacggc accgctggaa gtgggcgcag 180
 gtgactttct ggtgtccaga ggagcagctg tgtcacttgt ggctgcagac cctgcgggag 240
 atgctggaga agctgacgtc cagaccaaag catttactgg tatatatcaa cccgtttgga 300
 ggaaaaggac aaggcaagcg gatatatgaa agaaaagtgg caccactgtt caccttagcc 360
 tccatcacca ctgacatcat cggtaacaaa ttctatgtta actatgtaga agtaattact 420
 gaacatgcta atcaggccaa ggagactctg tatgagatta acatagacaa atacgacggc 480
 atcgtctgtg tcggcggaga tggatgttc agcaggtgct tgcacggctc gattgggagg 540
 acgcagagga gcgcccgggt cgaccagaac ccccccggt cctgtctggt cccagtagc 600
 ctccggattg gaatcattcc cgaggggtca acggactgct tgtgttactc caccgtgggc 660
 accagcgacg cagaaacctc ggcgtgtcat atcgttgttg gggactcgtt ggccatggat 720
 gtgtcctcag tccaccacaa cagcacactc ctctcgtact ccgtgtccct gctgggctac 780
 ggcttctacg gggacatcat caaggacagt gagaagaaac ggtggttggg tcttgccaga 840
 tacgactttt caggtttaaa gaccttcttc tcccaccact gctatgaagg gacagtgtcc 900
 ttcttccctg cacaacacac ggtgggatct ccaagggata ggaagccctg ccgggcagga 960
 tgttttgttt gcagggcaag caagcagcag ctggaggagg agcagaagaa agcactgtat 1020
 ggttttgaag ctgcggagga cgtggaggag tggcaagtct tctgtgggaa gtttctggcc 1080
 atcaatgcca caaacatgtc ctgtgtctgt cgccggagcc ccaggggcct ctccccggt 1140
 gccacttggt gagacgggtc ttctgacctc atcctcatcc ggaaatgctc caggttcaac 1200
 tttctgagat ttctcatcag gcacaccaac cagcaggacc agtttgactt cacttttgtt 1260
 gaagtttatc gcgtcaagaa attccagttt acgtcgaagc acatggagga tgaggacagc 1320
 gacctcaagg agggggggaa gaagcgtttt gggcacattt gcagcagcca cccctcctgc 1380
 tgtgcaccg tctccaacag ctcttgaac tgcgacgggt aggtcctgca cagccctgcc 1440
 atcgagggtca ggggtccactg ccagctgggt cgactctttg cagcaggaat tgaagagaat 1500

ccgaagccag actcacacag ctgagaagcc ggcgtcctgc tcacaaactg ggaaagtgtg 1560
 aaaactatatt aagataatta ttacagacca attatgttga tatatacatt taaatgtaga 1620
 aatttatattt tgatagttaa atcttgattt tagaagaaaa cccttttgtc aacaattttg 1680
 tgtacatatt tggcattttc agttctgtac gcatctgcgg gttgcagccc acgccgctta 1740
 ctctcagcaa gaaagaggtg gaggttgcgg tgagccaaga ttgcgccact gcactccagc 1800
 ctgggcaaac agagggagac tccatcgccc cccccaacaa 1840

<210> 6

<211> 471

<212> PRT

<213> Homo sapiens

<400> 6

Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys Val Lys Arg Ala Arg
 1 5 10 15

Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe Trp Cys Pro Glu Glu
 20 25 30

Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu Met Leu Glu Lys
 35 40 45

Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly
 50 55 60

Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu
 65 70 75 80

Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Gly Asn Lys Phe Tyr
 85 90 95

Val Asn Tyr Val Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu
 100 105 110

Thr Leu Tyr Glu Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val
 115 120 125

Gly Gly Asp Gly Met Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg
 130 135 140

Thr Gln Arg Ser Ala Gly Val Asp Gln Asn His Pro Arg Ala Val Leu
 145 150 155 160

Val Pro Ser Ser Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp
 165 170 175

Cys Val Cys Tyr Ser Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala
 180 185 190

Leu His Ile Val Val Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val
 195 200 205

His His Asn Ser Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr
 210 215 220

Gly Phe Tyr Gly Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu
 225 230 235 240

<400> 7						
gtggatatgt	caacataaatt	ggtcagtcga	aattttctta	agtaatatctc	acacttccca	60
aagctccttg	gctttgggat	tcttccttag	gactcttctt	cgatcccccg	agcaaagagg	120
tgcaccagct	ggcagttggac	cctgacctca	atggcagggc	tgtgcaggac	ttccccatca	180
cagttccagg	agcttctaga	ggttgggcga	gcgcaagggg	ggttgtcctt	gcagatctgc	240
ccaaacttct	gcttctctaq	ttccttcaa	tcattgtcat	catcttcac	gtgctttgat	300

gtgaactgga atttcttgac tcgataaact tcaacgaaag tgaagccaaa ctgacccctcc 360
 tgggttggtgt gccggatgag gaatctcagg aagttgaacc tggagcattt ccggataagg 420
 atgaggtcag aagacccatc tcccagatgg gcaaatgggg acaggccccc agggctccgg 480
 ggacaagcac aggacatgtt ggtggagttg atagccagga ac 522

<210> 8
 <211> 144
 <212> PRT
 <213> Rattus sp.

<400> 8
 Phe Leu Ala Ile Asn Ser Thr Asn Met Ser Cys Ala Cys Pro Arg Ser
 1 5 10 15
 Pro Gly Gly Leu Ser Pro Phe Ala His Leu Gly Asp Gly Ser Ser Asp
 20 25 30
 Leu Ile Leu Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu
 35 40 45
 Ile Arg His Thr Asn Gln Glu Asp Gln Phe Gly Phe Thr Phe Val Glu
 50 55 60
 Val Tyr Arg Val Lys Lys Phe Gln Phe Thr Ser Lys His Val Glu Asp
 65 70 75 80
 Asp Asp Asn Asp Leu Lys Glu Leu Glu Lys Gln Lys Phe Gly Gln Ile
 85 90 95
 Cys Lys Asp Asn Pro Pro Cys Ala Cys Pro Thr Ser Arg Ser Ser Trp
 100 105 110
 Asn Cys Asp Gly Glu Val Leu His Ser Pro Ala Ile Glu Val Arg Val
 115 120 125
 His Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Glu Ser
 130 135 140

<210> 9
 <211> 382
 <212> DNA
 <213> Mus musculus

<400> 9
 tttatcgagt caagaaatc cacttcacgt cgaagcacgt ggaagacgag gacaatgact 60
 cgaaggaaca agagaagcag aagtttggga agatctgcaa ggacagaccc tcttgactt 120
 gctcagcctc cagaagctcc tggaaactgcg atggcgaagt catgcacagc ccggccattg 180
 aggtcagggt ccactgccag ctggtgcgcc tctttgctcg gggaatcgag gaagagtcac 240
 aagcaagaac cccaaagccc accagctgtc ggccttgagc tcggggagtg tggaaattac 300
 ttaagaaaaa ttcgacagac cagttatgtt gatatatcca tttgaattta gaaatttatt 360
 tttgataggt aaatcttggg tt 382

<210> 10
 <211> 79

<212> PRT

<213> Mus musculus

<400> 10

Tyr Arg Val Lys Lys Phe His Phe Thr Ser Lys His Val Glu Asp Glu
1 5 10 15
Asp Asn Asp Ser Lys Glu Gln Glu Lys Gln Lys Phe Gly Lys Ile Cys
20 25 30
Lys Asp Arg Pro Ser Cys Thr Cys Ser Ala Ser Arg Ser Ser Trp Asn
35 40 45
Cys Asp Gly Glu Val Met His Ser Pro Ala Ile Glu Val Arg Val His
50 55 60
Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Glu Ser
65 70 75

<210> 11

<211> 326

<212> PRT

<213> Homo sapiens

<400> 11

Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly Gly Lys Gly Gln
1 5 10 15
Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu Phe Thr Leu Ala
20 25 30
Ser Ile Thr Thr Asp Ile Ile Gly Asn Lys Phe Tyr Val Asn Tyr Val
35 40 45
Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu
50 55 60
Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly
65 70 75 80
Met Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser
85 90 95
Ala Gly Val Asp Gln Asn His Pro Arg Ala Val Leu Val Pro Ser Ser
100 105 110
Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp Cys Val Cys Tyr
115 120 125
Ser Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala Leu His Ile Val
130 135 140
Val Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser
145 150 155 160
Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly
165 170 175

Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg
 180 185 190
 Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu
 195 200 205
 Gly Thr Val Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg
 210 215 220
 Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys
 225 230 235 240
 Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala
 245 250 255
 Ala Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala
 260 265 270
 Ile Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly
 275 280 285
 Leu Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu
 290 295 300
 Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu Ile Arg His
 305 310 315 320
 Thr Asn Gln Gln Asp Gln
 325

<210> 12
 <211> 453
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 12
 Leu Tyr Ile Asp Tyr Lys Pro His Ser Ser Ser His Leu Lys Glu Glu
 1 5 10 15
 Asp Asp Leu Val Glu Glu Ile Leu Lys Arg Ser Tyr Lys Asn Thr Arg
 20 25 30
 Arg Asn Lys Ser Ile Phe Val Ile Ile Asn Pro Phe Gly Gly Lys Gly
 35 40 45
 Lys Ala Lys Lys Leu Phe Met Thr Lys Ala Lys Pro Leu Leu Leu Ala
 50 55 60
 Ser Arg Cys Ser Ile Glu Val Val Tyr Thr Lys Tyr Pro Gly His Ala
 65 70 75 80
 Ile Glu Ile Ala Arg Glu Met Asp Ile Asp Lys Tyr Asp Thr Ile Ala
 85 90 95
 Cys Ala Ser Gly Asp Gly Ile Pro His Glu Val Ile Asn Gly Leu Tyr
 100 105 110

Gln Arg Pro Asp His Val Lys Ala Phe Asn Asn Ile Ala Ile Thr Glu
 115 120 125
 Ile Pro Cys Gly Ser Gly Asn Ala Met Ser Val Ser Cys His Trp Thr
 130 135 140
 Asn Asn Pro Ser Tyr Ser Thr Leu Cys Leu Ile Lys Ser Ile Glu Thr
 145 150 155 160
 Arg Ile Asp Leu Met Cys Cys Ser Gln Pro Ser Tyr Ala Arg Glu His
 165 170 175
 Pro Lys Leu Ser Phe Leu Ser Gln Thr Tyr Gly Leu Ile Ala Glu Thr
 180 185 190
 Asp Ile Asn Thr Glu Phe Ile Arg Trp Met Gly Pro Ala Arg Phe Glu
 195 200 205
 Leu Gly Val Ala Phe Asn Ile Ile Gln Lys Lys Lys Tyr Pro Cys Glu
 210 215 220
 Ile Tyr Val Lys Tyr Ala Ala Lys Ser Lys Asn Glu Leu Lys Asn His
 225 230 235 240
 Tyr Leu Glu His Lys Asn Lys Gly Ser Leu Glu Phe Gln His Ile Thr
 245 250 255
 Met Asn Lys Asp Asn Glu Asp Cys Asp Asn Tyr Asn Tyr Glu Asn Glu
 260 265 270
 Tyr Glu Thr Glu Asn Glu Asp Glu Asp Glu Asp Ala Asp Ala Asp Asp
 275 280 285
 Glu Asp Ser His Leu Ile Ser Arg Asp Leu Ala Asp Ser Ser Ala Asp
 290 295 300
 Gln Ile Lys Glu Glu Asp Phe Lys Ile Lys Tyr Pro Leu Asp Glu Gly
 305 310 315 320
 Ile Pro Ser Asp Trp Glu Arg Leu Asp Pro Asn Ile Ser Asn Asn Leu
 325 330 335
 Gly Ile Phe Tyr Thr Gly Lys Met Pro Tyr Val Ala Ala Asp Thr Lys
 340 345 350
 Phe Phe Pro Ala Ala Leu Pro Ser Asp Gly Thr Met Asp Met Val Ile
 355 360 365
 Thr Asp Ala Arg Thr Ser Leu Thr Arg Met Ala Pro Ile Leu Leu Gly
 370 375 380
 Leu Asp Lys Gly Ser His Val Leu Gln Pro Glu Val Leu His Ser Lys
 385 390 395 400
 Ile Leu Ala Tyr Lys Ile Ile Pro Lys Leu Gly Asn Gly Leu Phe Ser
 405 410 415

Val Asp Gly Glu Lys Phe Pro Leu Glu Pro Leu Gln Val Glu Ile Met
420 425 430

Pro Arg Leu Cys Lys Thr Leu Leu Arg Asn Gly Arg Tyr Val Asp Thr
435 440 445

Asp Phe Asp Ser Met
450

<210> 13

<211> 436

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 13

Leu Leu Ile Asp His Val Ser Arg Lys Ser Arg Ala Asn Thr Gly Glu
1 5 10 15

Glu Asn Ile Ser Ser Gly Thr Val Glu Glu Ile Leu Glu Lys Ser Tyr
20 25 30

Glu Asn Ser Lys Arg Asn Arg Ser Ile Leu Val Ile Ile Asn Pro His
35 40 45

Gly Gly Lys Gly Thr Ala Lys Asn Leu Phe Leu Thr Lys Ala Arg Pro
50 55 60

Ile Leu Val Glu Ser Gly Cys Lys Ile Glu Ile Ala Tyr Thr Lys Tyr
65 70 75 80

Ala Arg His Ala Ile Asp Ile Ala Lys Asp Leu Asp Ile Ser Lys Tyr
85 90 95

Asp Thr Ile Ala Cys Ala Ser Gly Asp Gly Ile Pro Tyr Glu Val Ile
100 105 110

Asn Gly Leu Tyr Arg Arg Pro Asp Arg Val Asp Ala Phe Asn Lys Leu
115 120 125

Ala Val Thr Gln Leu Pro Cys Gly Ser Gly Asn Ala Met Ser Ile Ser
130 135 140

Cys His Trp Thr Asn Asn Pro Ser Tyr Ala Ala Leu Cys Leu Val Lys
145 150 155 160

Ser Ile Glu Thr Arg Ile Asp Leu Met Cys Cys Ser Gln Pro Ser Tyr
165 170 175

Met Asn Glu Trp Pro Arg Leu Ser Phe Leu Ser Gln Thr Tyr Gly Val
180 185 190

Ile Ala Glu Ser Asp Ile Asn Thr Glu Phe Ile Arg Trp Met Gly Pro
195 200 205

Val Arg Phe Asn Leu Gly Val Ala Phe Asn Ile Ile Gln Gly Lys Lys
210 215 220

Tyr Pro Cys Glu Val Phe Val Lys Tyr Ala Ala Lys Ser Lys Lys Glu
 225 230 235 240
 Leu Lys Val His Phe Leu Glu Asn Lys Asp Lys Asn Lys Gly Cys Leu
 245 250 255
 Thr Phe Glu Pro Asn Pro Ser Pro Asn Ser Ser Pro Asp Leu Leu Ser
 260 265 270
 Lys Asn Asn Ile Asn Asn Ser Thr Lys Asp Glu Leu Ser Pro Asn Phe
 275 280 285
 Leu Asn Glu Asp Asn Phe Lys Leu Lys Tyr Pro Met Thr Glu Pro Val
 290 295 300
 Pro Arg Asp Trp Glu Lys Met Asp Ser Glu Leu Thr Asp Asn Leu Thr
 305 310 315 320
 Ile Phe Tyr Thr Gly Lys Met Pro Tyr Ile Ala Lys Asp Thr Lys Phe
 325 330 335
 Phe Pro Ala Ala Leu Pro Ala Asp Gly Thr Ile Asp Leu Val Ile Thr
 340 345 350
 Asp Ala Arg Ile Pro Val Thr Arg Met Thr Pro Ile Leu Leu Ser Leu
 355 360 365
 Asp Lys Gly Ser His Val Leu Glu Pro Glu Val Ile His Ser Lys Ile
 370 375 380
 Leu Ala Tyr Lys Ile Ile Pro Lys Val Glu Ser Gly Leu Phe Ser Val
 385 390 395 400
 Asp Gly Glu Lys Phe Pro Leu Glu Pro Leu Gln Val Glu Ile Met Pro
 405 410 415
 Met Leu Cys Lys Thr Leu Leu Arg Asn Gly Arg Tyr Ile Asp Thr Glu
 420 425 430
 Phe Glu Ser Met
 435

<210> 14
 <211> 380
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 14
 Cys Trp Val Asp Phe Val Glu Asn Ser Asp Gln Phe Cys Glu Tyr Leu
 1 5 10 15
 Leu Asp Val Ala Tyr Lys Gly Ile Lys Arg Ser Arg Arg Phe Ile Val
 20 25 30
 Phe Ile Asn Pro His Gly Gly Lys Gly Lys Ala Lys His Ile Trp Glu
 35 40 45

Ser Glu Ala Glu Pro Val Phe Ser Ser Ala His Ser Ile Cys Glu Val
 50 55 60
 Val Leu Thr Arg Arg Lys Asp His Ala Lys Ser Ile Ala Lys Asn Leu
 65 70 75 80
 Asp Val Gly Ser Tyr Asp Gly Ile Leu Ser Val Gly Gly Asp Gly Leu
 85 90 95
 Phe His Glu Val Ile Asn Gly Leu Gly Glu Arg Asp Asp Tyr Leu Glu
 100 105 110
 Ala Phe Lys Leu Pro Val Cys Met Ile Pro Gly Gly Ser Gly Asn Ala
 115 120 125
 Phe Ser Tyr Asn Ala Thr Gly Gln Leu Lys Pro Ala Leu Thr Ala Leu
 130 135 140
 Glu Ile Leu Lys Gly Arg Pro Thr Ser Phe Asp Leu Met Thr Phe Glu
 145 150 155 160
 Gln Lys Gly Lys Lys Ala Tyr Ser Phe Leu Thr Ala Asn Tyr Gly Ile
 165 170 175
 Ile Ala Asp Cys Asp Ile Gly Thr Glu Asn Trp Arg Phe Met Gly Glu
 180 185 190
 Asn Arg Ala Tyr Leu Gly Phe Phe Leu Arg Leu Phe Gln Lys Pro Asp
 195 200 205
 Trp Lys Cys Ser Ile Glu Met Asp Val Val Ser Ser Asp Arg Thr Glu
 210 215 220
 Ile Lys His Met Tyr Glu Lys Ser Lys Asn Leu Ala Pro Met Ser Glu
 225 230 235 240
 Ser Ser Asp Ser Asp Lys Thr Val Ser Thr Ser Pro Glu Ser His Leu
 245 250 255
 Leu Thr Phe Glu Ile Asn Asp Leu Ser Ile Phe Cys Ala Gly Leu Leu
 260 265 270
 Pro Tyr Ile Ala Pro Asp Ala Lys Met Phe Pro Ala Ala Ser Asn Asp
 275 280 285
 Asp Gly Leu Ile Asp Val Val Ile Val Tyr Ser Lys Gln Phe Arg Lys
 290 295 300
 Ser Leu Leu Ser Met Phe Thr Gln Leu Asp Asn Gly Gly Phe Tyr Tyr
 305 310 315 320
 Ser Lys His Leu Asn Tyr Tyr Lys Val Arg Ser Phe Arg Phe Thr Pro
 325 330 335
 Val Asn Thr Gly Lys Arg His Tyr Phe Ala Leu Asp Gly Glu Ser Tyr
 340 345 350
 Pro Leu Glu Pro Phe Glu Cys Arg Val Ala Pro Lys Leu Gly Thr Thr

355 360 365
 Leu Ser Pro Val Ala Gly Phe Gln Leu Leu Asp Ile
 370 375 380

 <210> 15
 <211> 415
 <212> PRT
 <213> Caenorhabditis elegans

 <400> 15
 Cys Arg Ser Asp Ala Glu Glu Asn Glu Gln Leu Thr Ser Val Ile Leu
 1 5 10 15
 Ser Arg Lys Pro Pro Pro Gln Glu Gln Cys Arg Gly Asn Leu Leu Val
 20 25 30
 Phe Ile Asn Pro Asn Ser Gly Thr Gly Lys Ser Leu Glu Thr Phe Ala
 35 40 45
 Asn Thr Val Gly Pro Lys Leu Asp Lys Ser Leu Ile Arg Tyr Glu Val
 50 55 60
 Val Val Thr Thr Gly Pro Asn His Ala Arg Asn Val Leu Met Thr Lys
 65 70 75 80
 Ala Asp Leu Gly Lys Phe Asn Gly Val Leu Ile Leu Ser Gly Asp Gly
 85 90 95
 Leu Val Phe Glu Ala Leu Asn Gly Ile Leu Cys Arg Glu Asp Ala Phe
 100 105 110
 Arg Ile Phe Pro Thr Leu Pro Ile Gly Ile Val Pro Ser Gly Ser Gly
 115 120 125
 Asn Gly Leu Leu Cys Ser Val Leu Ser Lys Tyr Gly Thr Lys Met Asn
 130 135 140
 Glu Lys Ser Val Met Glu Arg Ala Leu Glu Ile Ala Thr Ser Pro Thr
 145 150 155 160
 Ala Lys Ala Glu Ser Val Ala Leu Tyr Ser Val Lys Thr Asp Asn Gln
 165 170 175
 Ser Tyr Ala Ser Phe Leu Ser Ile Gly Trp Gly Leu Met Ala Asp Ile
 180 185 190
 Asp Ile Asp Ser Glu Lys Trp Arg Lys Ser Leu Gly His His Arg Phe
 195 200 205
 Thr Val Met Gly Phe Ile Arg Ser Cys Asn Leu Arg Ser Tyr Lys Gly
 210 215 220
 Arg Leu Thr Tyr Arg Pro Tyr Lys Pro Lys Gly Phe His Pro Ser Ser
 225 230 235 240
 Asn Val Phe Ser Val Tyr Glu Lys Thr Thr Gln Gln Arg Ile Asp Asp

	245		250		255
Ser Lys Val	Lys Thr Asn Gly Ser Val Ser Asp Ser Glu Glu Glu Thr				
	260		265		270
Met Glu Thr	Lys Phe Gln Asn Trp Thr Leu Pro Asp Ser Asp Glu Thr				
	275		280		285
Leu Ala Val	Gly Ser Ser Asp Leu Glu Glu Thr Val Val Ile Glu Asp				
	290		295		300
Asn Phe Val	Asn Ile Tyr Ala Val Thr Leu Ser His Ile Ala Ala Asp				
	305		310		315
Gly Pro Phe	Ala Pro Ser Ala Lys Leu Glu Asp Asn Arg Ile His Leu				
	325		330		335
Ser Tyr Ile	Leu Trp Lys Asp Ile Gly Thr Arg Val Asn Ile Ala Lys				
	340		345		350
Tyr Leu Leu	Ala Ile Glu His Glu Thr His Leu Asp Leu Pro Phe Val				
	355		360		365
Lys His Val	Glu Val Ser Ser Met Lys Leu Glu Val Ile Ser Glu Gly				
	370		375		380
Ser His Val	Val Leu Asp Gly Glu Val Val Asp Thr Lys Thr Ile Glu				
	385		390		395
Val Ala Ser	Thr Lys Asn His Ile Ser Val Phe Ser Ser Thr Ala				
	405		410		415

<210> 16
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Illustrative motif

<400> 16
 Asn Glu Gln Lys
 1

<210> 17
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Illustrative motif

<400> 17
 Asn His Gln Lys

1

<210> 18
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
motif

<400> 18
Asn Asp Glu Gln
1

<210> 19
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
motif

<400> 19
Gln His Arg Lys
1

<210> 20
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
motif

<400> 20
Met Ile Leu Val
1

<210> 21
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
motif

<400> 21
Met Ile Leu Phe
1

<210> 22
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative motif

<400> 22
Ser Thr Asn Lys
1

<210> 23
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative motif

<400> 23
Ser Thr Pro Ala
1

<210> 24
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative motif

<400> 24
Ser Gly Asn Asp
1

<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative motif

<400> 25
Ser Asn Asp Glu Gln Lys
1 5

<210> 26

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative motif

<400> 26
Asn Asp Glu Gln His Lys
1 5

<210> 27
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative motif

<400> 27
Asn Glu Gln His Arg Lys
1 5

<210> 28
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative motif

<400> 28
Val Leu Ile Met
1

<210> 29
<211> 132
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 80432911

<400> 29
Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser Glu Ile
1 5 10 15
Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly Ser Gly
20 25 30
Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys Val
35 40 45

Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe Trp
50 55 60

Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu
65 70 75 80

Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile
85 90 95

Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys
100 105 110

Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Val
115 120 125

Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn Ile
130 135 140

Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly Met Phe Ser
145 150 155 160

Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser Ala Gly Val
165 170 175

Asp Gln Asn His Pro Arg
180